EXHIBIT A

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                        1                                              50
gls (2247)      (1)   MVAFESLWPQNLSCTRVYSAKEIESLDSYLTMPIPEYLHEILDDVRDTTS
GLSA_CORGL      (1)   ------------------------------MLTMPIPEYLHEILDDVRDTTS
GLSA_COREF      (1)   -----------------------MTTHPLTMPIPEYFEEILESVRSDVS
GLSA1_BRAJA     (1)   -------------------TIPPPASAWTRSKP-PLLRFLDTCLNIFSAETS
GLSA2_BRAJA     (1)   -------MDTQPIRLPSYAGATRSAGYPTRP-PLRRFLTICHEEFRGDSS
GLSA_ANASP      (1)   ------------------TSDQANQGDLEIRPSPLLKVINDIHSKYKSLKE
Consensus       (1)                      MS    SA    MLTMPIPEYL EILDDVRSDTS

                        51                                             100
gls (2247)     (51)   GELADYIPELKSADPNPLAVALCTVNGHIYSAGDDDIEFTMQSISKPFAY
GLSA_CORGL     (23)   GELADYIPELKSADPNPLAVALCTVNGHIYSAGDDDIEFTMQSISKPFAY
GLSA_COREF     (27)   GEVAGYIPQLKDADPNPLALAMCTVDGHIYGAGDDEHEFTMQSVSKPFAY
GLSA1_BRAJA    (33)   GAVADYIPELGNADPAYFGISLATLDGHVYEVGDSRVPFTIQSMSKPFVF
GLSA2_BRAJA    (43)   GELADYIPELKRANPDHFGIALVTLDGHVYEVGDSAVPFTIQSVSKAFVF
GLSA_ANASP     (34)   GIVANYIPELAKVNPDLFSISIVTVDGQVYQVGDYQQLFTLQSISKVFAY
Consensus      (51)   GELADYIPELK ADPNPLATALCTVDGHIY VGDDDIEFTIQSISKPFAY

                        101                                            150
gls (2247)    (101)   ALALQECGFDEVSASVALEPSGEAFNELSLDG-ENRPMNPMINAGAIAIN
GLSA_CORGL     (73)   ALALQECGFDEVSASVALEPSGEAFNELSLDG-ENRPMNPMINAGAIAVN
GLSA_COREF     (77)   ALALQEQGPEKVFAIVGLEPSGEAFNELSLDGSTNRPMNPMINAGAIACT
GLSA1_BRAJA    (83)   ALALDLLGAGRVESALGVEPSGDPFNSIRLNSDN-HPFNPMVNAGAIACT
GLSA2_BRAJA    (93)   ALALETVGEERVSATIGVEPSGEAFNSIRLTNDN-RPFNPMVNAGAIACS
GLSA_ANASP     (84)   GLALEDHGRDYVLTRVGVEPTGEAFNAIILDEQSKRPYNPMVNAGAIATT
Consensus     (101)   ALALQE G DRVSASVGLEPSGEAFNEISLDG  NRPMNPMINAGAIAIN

                        151                                            200
gls (2247)    (150)   QLINGSDSTVEDRVEKIRHYFSELAGRELTIDRVLAESELAGADRNLSIA
GLSA_CORGL    (122)   QLINGSDSTVEDRVEKIRHYFSELAGRELTIDRVLAESELAGADRNLSIA
GLSA_COREF    (127)   QLINGSESSVEDRVEKIRSYFSALAGRELNIDRQESETEIEGADRNLSIA
GLSA1_BRAJA   (132)   GLIYDSKG--AEAFEQIRLALSRFAGRDLAVDEAVYSSESQTGDRNRAIG
GLSA2_BRAJA   (142)   GLIYEVDG--KGAFERVRSKLSEFAGRELGVDEAVHASETATGNRNRAIA
GLSA_ANASP    (134)   SLIKGAGA--TERENRVLEMRRYIGHDVFVDISVFTSERSTGHRNRAMA
Consensus     (151)   QLINGSDSTVEDRVEKIR YFSELAGREL IDRALAESELATADRNRAIA

                        201                                            250
gls (2247)    (200)   HMLRNYGVIEDEAHDAVLSYTLQCAIKVTIRDLAVMTATLAAGGTHPITG
GLSA_CORGL    (172)   HMLRNYGVIEDEAHDAVLSYTLQCAIKVTIRDLAVMTATLAAGGTHPITG
GLSA_COREF    (177)   HMLRNYGIIEDDAHDAVLSYTLQCSVKVTARDLAVMTATLAAGGTQPLTG
GLSA1_BRAJA   (180)   YLLKTNAVISDNVAAVDVYFRQCAVLVTARDIAVMAATLANRGIINPVTG
GLSA2_BRAJA   (190)   WLLRNYAVLPDDVDAVLDVYFRQCAILVTARDLAVMAATLANRGIINPVTG
GLSA_ANASP    (182)   HLMLNFGMIDRNIEEAIDLYFGQCAVMVNCHDLAVMAATLANRGVNPITG
Consensus     (201)   HLLRNYGVIEDDAHDALLSYTLQCAIKVTARDLAVMTATLANRGTNPITG

                        251                                            300
gls (2247)    (250)   KKLLDARVCRLTLSVMASAGMYDEAGQWLSTVGIPAKSGVAGGLIGILPG
GLSA_CORGL    (222)   KKLLDARVCRLTLSVMASAGMYDEAGQWLSTVGIPAKSGVAGGLIGILPG
GLSA_COREF    (227)   EKLVDARVARLVLSTMASAGMYDEAGQWLATVGIPAKSGVSGGLVGVLPG
GLSA1_BRAJA   (230)   EGVISAYAISRTLSVMTSSGMYDYAGEHIYRIGIPAKSGVGGGIILAALPA
GLSA2_BRAJA   (240)   AQVITPHIVARTLSVMTSSGMYDYAGEHTYRVGIPAKSGVGGGIVAALPS
GLSA_ANASP    (232)   EQAVNSRYIKDTLSVMYTCGMYNFAGEHAVKVGIPAKSGVCGGIIAVVPN
Consensus     (251)   EQLLDARVIRLTLSVMASAGMYDEAGQWLYTVGIPAKSGVAGGIIAILPG

                        301                                            350
gls (2247)    (300)   QLGIATFSPRLNPKGNSVRGVKIFKQLSDDMGLHLMSTEQVSGHAVRSIT
GLSA_CORGL    (272)   QLGIATFSPRLNPKGNSVRGVKIFKQLSDDMGLHLMSTEQVSGHAVRSIT
GLSA_COREF    (277)   QLGIATFSPRLNSQGNPVRGVEIFKALSEDMGLHLMSAELUTQHAVRAIE
GLSA1_BRAJA   (280)   RLEGLGSYSPKLDKHGNSVRGIKVCEALSSHYDLHMLNRSDDARNAVIADY
GLSA2_BRAJA   (290)   QLGLGTFSPLLDNHFNSVRGLKVCEALSARFDLHMLNRNADVRTSVMADY
GLSA_ANASP    (282)   LMGIIAVFSPPLDIRGNSVRGVKVCEELSQQEGLHLFECMKVGNGEWGVGN
Consensus     (301)   QLGIATFSPRLN KGNSVRGVKIFKALSDDMGLHLMS E VS HAVRAI

                        351                                            400
gls (2247)    (350)   RDG--------------------DTTFIQMQGAMNFSASESFLHAIVEH
GLSA_CORGL    (322)   RDG--------------------DTTFIQMQGAMNFSASESFLHAIVEH
GLSA_COREF    (327)   ERG--------------------DTTVIQLQLGAMNFSAAENFLFTVTDH
GLSA1_BRAJA   (330)   DIGKSPSRRVVRRAQEREILAAHEQEVRIIELVGTLSLSAVDYVSRRLAGR
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GLSA2_BRAJA   (340)  IVYGISSRRSRQPHEQQILDERHSDIRIVELVGALNFGTIDYVTRRITSE
GLSA_ANASP    (332)  CIC-----------------------------------------------
Consensus     (351)  DDG                      DTTIIQLQGAMNFSASE FL  I EH
                     401                                            450
   gls(2247)  (379)  NFEGTEVVLDLTRVLSFHPVAIRMIKEGLKRIRDAGFEVFILDPDDVLPD
GLSA_CORGL    (351)  NFEGTEVVLDLTRVLSFHPVAIRMIKEGLKRIRDAGFEVFILDPDDVLPD
GLSA_COREF    (356)  DFTGEKVVLDLSRVPMFRPMGRRLVKEGLRRIRDNGFKVAIYDPEDILPD
GLSA1_BRAJA   (380)  P-RPQFVIFDLHRVTSTTRAGARLVAEAFEELAALNVTVVESGVRRASKE
GLSA2_BRAJA   (390)  PPNAPLERIDFRRVPDITAAGAELLGETLTAIGNANVTTIESGLEEASAV
GLSA_ANASP    (335)  -------------------------------------------------
Consensus     (401)   F G  VVLDLTRV SF PVG RLIKEGLKRIRDAGF V I DPDDVLPD
                     451                                            500
   gls(2247)  (429)  FMFSDGTIICKERV------------------------------------
GLSA_CORGL    (401)  FMFSDGTIICKERV------------------------------------
GLSA_COREF    (406)  FDFSDGTKSPQVDDPEEL-------------------------------
GLSA1_BRAJA   (429)  INTLREWTAELKNVRDFYLLDTAIEWAEDQIVYRYGGSIDFHETTELAEQ
GLSA2_BRAJA   (440)  IAAIARTGDPRRLRRFALLDDAIEWAEDQVIYRFGGFTDVKESVHLGEQ
GLSA_ANASP    (335)  -------------------------------------------------
Consensus     (451)  F FSDGT    R
                     501                                            550
   gls(2247)• (442)  -------------------------------------------------
GLSA_CORGL    (414)  -------------------------------------------------
GLSA_COREF    (424)  -------------------------------------------------
GLSA1_BRAJA   (479)  PLLEGLSADELAELGAICTIRTYQSGAKILTTGDPADALFFLRSGAVHVT
GLSA2_BRAJA   (490)  ALLAELDTDEIAAIVKLSTTRHYTAGQRVIAAGAPANSLFFLQSGMVSVK
GLSA_ANASP    (335)  -------------------------------------------------
Consensus     (501)
                     551                                            600
   gls(2247)  (442)  -------------------------------------------------
GLSA_CORGL    (414)  -------------------------------------------------
GLSA_COREF    (424)  -------------------------------------------------
GLSA1_BRAJA   (529)  LPDGVRLATLTAGMAFGEMALLEQTRSADVFADMAATAFEAPLKDFERFR
GLSA2_BRAJA   (540)  LRSGVRLASLGPGMEFGEMAILERTRSADVFADTPVACLELPLDSFADYR
GLSA_ANASP    (335)  -------------------------------------------------
Consensus     (551)
                     601                        635
   gls(2247)  (442)  ---------------------------------
GLSA_CORGL    (414)  ---------------------------------
GLSA_COREF    (424)  ---------------------------------
GLSA1_BRAJA   (579)  EQHPRASERIMRNLAQLLADRLIVANAKVDILTST
GLSA2_BRAJA   (590)  RLHPETALKIMRNLAAILARRLVAANAKVDLLSAY
GLSA_ANASP    (335)  ---------------------------------
Consensus     (601)
```

GLSA_CORGL : Q8NMT3; Corynebacterium glutamicum
GLSA_COREF : Q8FMX4; Corynebacterium efficiens.
GLSA1_BRAJA : Q89NA7; Bradyrhizobium japonicum,
GLSA2_BRAJA : Q89KV2; Bradyrhizobium japonicum
GLSA_ANASP : Q8YSZ5; Anabaena sp. (strain PCC 7120)

2

EXHIBIT B

Alignment of nucleotide sequences of glutamine synthetase genes

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                    1                                                50
2247        (1)   --------------GTGGCGTTTGAA-ACCCCGGAAGAAATTGTCAAGTT
13032       (1)   --------------GTGGCGTTTGAA-ACCCCGGAAGAAATTGTCAAGTT
CEFglnA1    (1)   --------------GTGGCGTTTAAC-ACCCCGGAAGAAGTAACCAAGTT
CEFglnA2    (1)   ------GTGGCCTCGAGCCCGACAACCAACCCGGATGAGATCCTCAAGTT
MtuglnA2    (1)   ------------------ATGGACCGACAGAAGGAATTCGTTCTTCG
MtuglnA3    (1)   ---------------ATGACAGCCACACCGCTTGCCGCGGCCGCGAT
MtuglnA4    (1)   GTGACCGGCCCCGGTTCGCCGCCGTTGGCGTGGACCGAGTTGGAGCGACT
MtuglnA1    (1)   ------------GTGACGGAAAAG-ACGCCCGACACGTCTTCAAACT
Consensus   (1)                 GTGGCGGATGA ACCCCGGA GAA T GTCAAGTT

                    51                                               100
2247        (36)  CATCA---AGGATGAA--AACGTCGAGTTCGTTGACGTTCGATTCACCG
13032       (36)  CATCA---AGGATGAA--AACGTCGAGTTCGTTGACGTTCGATTCACCG
CEFglnA1    (36)  CATCA---AGGATGAA--AACGTTGAGTTCGTCGATGTCCGATTCACCG
CEFglnA2    (45)  CATCC---GGGACAAT--GACATCAACTGGGTGGACGTCCAGTTCACCG
MtuglnA2    (30)  TACCC---TGGAAGAACGCGACATCCGCTTCGTCCGGCTGTGGTTCACAG
MtuglnA3    (33)  CGCCCAATTGGAGGCAGAGGGCGTCGACACCGTCATCGGCACCGTCGTGA
MtuglnA4    (51)  GGTCG---CGGCCGGT--GACGTCGACACCGTCATCGTCGCGTTCACCG
MtuglnA1    (36)  TGCCA---AGGACGAG--AAGGTCGAATATGTCGACGTCCGGTTCTGTG
Consensus   (51)  CATCA   AGGA GAA   GACGTCGACTTCGTCGACGTCCGGTTCACCG

                    101                                              150
2247        (80)  ACCTTCCCGGCACCGAGCAGCACTTCAGCATCCCAGCTGCCAGCTTCGAT
13032       (80)  ACCTTCCCGGCACCGAGCAGCACTTCAGCATCCCAGCTGCCAGCTTCGAT
CEFglnA1    (80)  ACCTTCCCGGAATCGAGCAGCACTTCAGCATCCCCGCATCCGCTCTTGAT
CEFglnA2    (89)  ACGTTCCCGGCACCGAACAGCACCTGTCCGTGCCCGCCGCGGCATTCGAC
MtuglnA2    (77)  ACGTGCTCGGTTTCCTCAAGTCGGTCGCCATCGCCCCAGCCGAACTCGA
MtuglnA3    (83)  ACCCCGCCGGACTCACCCAGGCCAAGACCGTGCCGATACGCCGGACCAA-
MtuglnA4    (95)  ACATGCAGGGC------CGGCTGGCCGGCAAACGGATATCGGGGCGGCA-
MtuglnA1    (80)  ACCTGCCTGGCATCATGCAGCACTTCACGATTCCGGCTTCGGCCTTTGAC
Consensus   (101) ACCTTCCCGGCATCGAGCAGCACTTCAGCATCCC GCAGCCGGCTTCGA

                    151                                              200
2247        (130) GCAGATACAGTCGAAGAAGGTCTCGGCATTCGACGGATCCTCGATCCGTGG
13032       (130) GCAGATACAAATCGAAGAAGGTCTCGGCATTCGACGGATCCTCGATCCGTGG
CEFglnA1    (130) GAGGACGCCATCGAGGAGGGCCTCGCCTTCGACGGTTCCTCCATCCGTGG
CEFglnA2    (139) GAATCCGCCATGGAAACGGACTGGCCTTCGACGGGTCATCGATCAGCGG
MtuglnA2    (126) --GGGCGCCTTCGAGGAAGGCATCGGCTTCGACGGATCCTCGATCGAGGG
MtuglnA3    (132) ------CACAATTCGCCAA--TCCTGGCCT-CGGCGCCAGTCCGGTGTGGCA
MtuglnA4    (138) -------T--TTCGTCGACGACATAGCCACCGCGCGGCGTCGAGTGCTGCAG
MtuglnA1    (130) AAGAGCGTGTTTGACGACGGCTTCGGCCTTTGACGGCCTCGTCGATTCGCGG
Consensus   (151) G  G CGC TTCGA GA GGCCTCGCCTTCGACGG TCCTCGATCCG GG

                    201                                              250
2247        (180) CTTCACCACGATCGACGAATCTGACATGAATCTCCTGCCAGACCTC-GGA
13032       (180) CTTCACCACGATCGACGAATCTGACATGAATCTCCTGCCAGACCTC-GGA
CEFglnA1    (180) TTTCACCACCATTGATGAATCCGACATGAACCTGCTGCCGGATCTG-GCC
CEFglnA2    (189) ATACACCACTGTCGACCATTCCGACATGATGCTGCTGCCGGATCTG-TCC
MtuglnA2    (174) CTTTGCGCGGGTCTCGGAATCCGATACGGTGGCGCACCCGGACC------
MtuglnA3    (174) TACGTTCTGTATCGACCAATGCAGTATTGCATTCACCGCAGACATCAGTG
MtuglnA4    (180) TTATCTGCTGGCCGTGGACGTCGACCTGAACACGGTGCCCGGCTAT-GCG
MtuglnA1    (180) GTTCCAGTCGATCCACGAATCCGACATGTTGCTTCTTCCCGATCCC-GAG
Consensus   (201) TTCACCACGATCGACGAATCCGACATGAA CTGCTGCC GACCTC G

                    251                                              300
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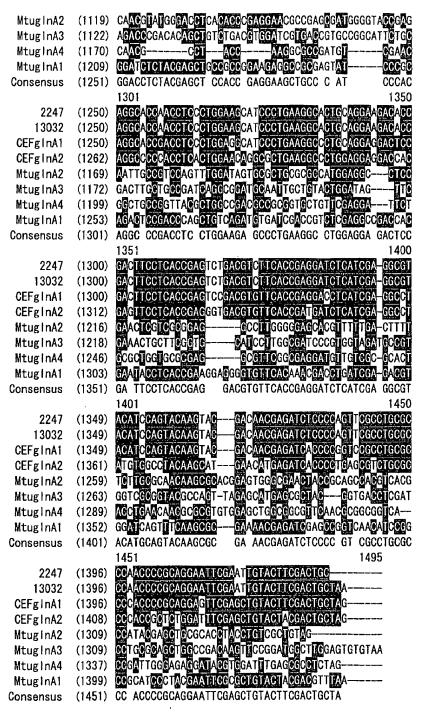
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2247        (229)  ACGGCCACCCTTGATCC---ATTCCGCAA-----GGCAAAGACCCTGAACGT
13032       (229)  ACGGCCACCCTTGATCC---ATTCCGCAA-----GGCAAAGACCCTGAACGT
CEFglnA1    (229)  ACCGCGAAGATCGATCC---GTTCCGCAA-----GGCGAAGACCCTGAACAT
CEFglnA2    (238)  ACGGCGTTCATCGACCC---GTTCCGCAG-----GTCGAAGACGCTCAACAT
MtuglnA2    (218)  -CGTCGACCTTCCAGGT--GCTGCCCTG-----GGCCA----CC-------
MtuglnA3    (224)  TGGTCGGCGATCAACGT---CTCCGCAT-------CGA----TC-------
MtuglnA4    (229)  ATGGCCAGTTGGGACACCGGCTACGGCGATATGGTGATGACGCCGGACTT
MtuglnA1    (229)  ACGGCGCGCATCGACCC--GTTCCGCGC-----GGCCAAGACGCTGAATAT
Consensus   (251)  ACGGCGACCATCGACCC  GTTCCGCA    GGCGAAGACCCTGAAC T
                   301                                              350
2247        (273)  -TAAGTTCTTCGTTCACGATCCTTTCACCCGCGAGGCATTCTCCCGCGAC
13032       (273)  -TAAGTTCTTCGTTCACGATCCTTTCACCCGCGAGGCATTCTCCCGCGGAC
CEFglnA1    (273)  -CAAGTTCTTCGTCCATGACCCCTTCACCCGTGAGGCGTTCTCCCGCGAC
CEFglnA2    (282)  -CAAGTTCTTCGTCCATGACCCCTATACCCGGGAACCATTTTCCCGGGGAT
MtuglnA2    (250)  ---AGTTC--CGGCCACCACCACT-CAGCGCGGATGTTTTGCGACATCA-
MtuglnA3    (254)  -T--GTCCGCCTTGCCCATCATCGGCGACGGGTTGGCGTG--GGCGCCCG
MtuglnA4    (279)  GTCCACTCTGCGGCTGATTCCTTGGCTACCGGGAACGGCGCTGGTGATCG
MtuglnA1    (273)  -CAACTTCTTTGTGCACGACCCCGTTCACCCTGGAGCCGTACTCCCGCGAC
Consensus   (301)  TAAGTTCTTCGTCCACGACCCCTTCACCCGGGAGGCGTTCTCCCGCGAC
                   351                                              400
2247        (322)  CCACGCAACGTAGCACGCAAGGCAGAGCAGTACCTGGC----ATCCACCGG
13032       (322)  CCACGCAACGTGGCACGCAAGGCAGAGCAGTACCTGGC----ATCCACCGG
CEFglnA1    (322)  CCCCGCAATGTGGCACGTAAGGCCGAGCAGTTCCTGGC----GTCCACCGG
CEFglnA2    (331)  CCCCGCAACATCGCCCGCAAGGCGGAGGAGTACCTGGC----TTCCACCGG
MtuglnA2    (293)  CCATGCCGGACGGCTCGCC-GTCGTGGGCGGACCCG------CGGCACGTG
MtuglnA3    (299)  CCGGGTTCTTCGAGCAGGACGGCACACCGGTCCCCGC----CTGCAGCCCG
MtuglnA4    (329)  CCGACCTGGTCTGGGCCGACGGCAGCGAGGTCGCCGTCTCGCGCGCGCAGC
MtuglnA1    (322)  CCGCGCAACATCGCCCGCAAGGCCGAGAACTACCTGAT---CAGCACTGG
Consensus   (351)  CC CGCAAC TGGC CGCAAGGCAGAGCAGTACCTGGC    CTGCACCGG
                   401                                              450
2247        (369)  CATTGCAGACACCTGCAACTTCGGCGCCGAGGGCTGAGTTCTACCTCTTCG
13032       (369)  CATTGCAGACACCTGCAACTTCGGCGCCGAGGGCTGAGTTCTACCTCTTCG
CEFglnA1    (369)  CATCGCCGACACCTGCAACTTCGGCGCCGAGGGCCGAGTTCTATCTCTTCG
CEFglnA2    (378)  TTTCGCCGACAGCTGTAACTTCGGCGCCGAAGGCCGAGTTCTACATCTTCG
MtuglnA2    (337)  TTGCGGCGGCAGCTG--ACGAAGGC--G--GGCGAACTCGGCTTCTCCT
MtuglnA3    (345)  AGGAACACTGAGCCGGATCGAGGCCCGCGCTTGCTGATGCCCGCATCGACG
MtuglnA4    (379)  ATTCTGCGCCGTCAGCTCGATCGGCT-CAAGGC--GCGCGGACTGGTCG
MtuglnA1    (369)  CATCGCCGACACCGCATACTTCGGCGCCGAGGGCCGAGTTCTACATTTTCG
Consensus   (401)  CATCGCCGACACCTGCAACTTCGGCGCCGAGGC GAGTTCTACCTCTTCG
                   451                                             ·500
2247        (419)  ACTCCGTTCGCTACTCCACCGAGATGAACTCCGGCTTTCTACGAAGTAGAT
13032       (419)  ACTCCGTTCGCTACTCCACCGAGATGAACTCCGGCTTTCTACGAAGTAGAT
CEFglnA1    (419)  ACTCCGTCCGTTACTCCACCGACATCAACTCCGGTTTTCTACCATGTGGAC
CEFglnA2    (428)  ACTCCGTGCGGTTCAGCTCCCAGTCCAATGCGGCATTCCACGAGGTGGAT
MtuglnA2    (380)  GCTACGTGCATCCCGAAATCGAG------------TTCTTGCTGCTCAAG
MtuglnA3    (395)  CGGTAATCGGGCACGAAGTGGAA------------TTCCTCTTGGTCGAC
MtuglnA4    (425)  CCGATGTGGCCACCGAGCTGGAGTTCATCGT-G--TTCGACCAGCCGTAT
MtuglnA1    (419)  ATTCGGTGAGCTTCGACTCGCGCGCCAACGGCTCCTTCTACGAGGTGGAC
Consensus   (451)  ACTCCGTGCGCTACGACACCGAG TCAAC CCG TTCTACGAGGTGGAT
                   501                                              550
2247        (469)  ACCGAAGAAGGCTGGTGGAACCGTGGCAAGGAAACCAACCTCGACGGGAAC
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2

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     13032   (469) ACCGAAGAAGGCTGGTGGAACCGTGGCAAGGAAACCAACCTCGACGGCAC
  CEFgInA1   (469) ACCAACGAGGGTTGGTGGAACCGTGGCCGTGAGACCAACCTCGATGGCAC
  CEFgInA2   (478) TCCGTGGAGGGCTGGTGGAACAGTGGTTCCCGGGAGAACCCGGACGGCAG
  MtugInA2   (418) CCC---------GGACCCGAGGACGGG----------TCGGTGCCCG
  MtugInA3   (433) GCGGA------C---G-GCCAGCGGCTGCCT-------TCGACG-CTG
  MtugInA4   (472) CGCC----AGGCA-TGGGCCAGCGG---GTA-------TCGCGGGCTG
  MtugInA1   (469) GCCATCTCGGGGTGGTGGAACACCGGCGCGGCGACCGAGGCCGACGGCAG
 Consensus   (501) CCGA GAGGGCTGGTGGAACCGTGGC  GGA ACCAACCTCGACGGCAG
                   551                                            600
      2247   (519) CCCAAACCTGGGCGCAAAGAACCGCGTCAAGGGTGGCTACTTCCCAGTAG
     13032   (519) CCCAAACCTGGGCGCAAAGAACCGCGTCAAGGGTGGCTACTTCCCAGTAG
  CEFgInA1   (519) CCCCAACACCGGTTCCAAGAACCGCCTCAAGGGCGGTTACTTCCCCGTCG
  CEFgInA2   (528) CAGGAACCTGGGTCACAAGGTACGGCAGAAGGGTTGGTTACTTCCCGGTGG
  MtugInA2   (446) TCCC----GGTCG--A--------CAACGCCGGCTATTTCGACCAAG
  MtugInA3   (463) T--------GGGC----GC--------AGTACGG----TGTCGGCGGGGG
  MtugInA4   (505) ACCC-----C-GGCC----AGCGA-----CTACAACATCGACTACGCGATATTGG
  MtugInA1   (519) TCCCAACCGGGGGCTACAAGGTCCGCCACAAGGGGCGGGTATTTCCCAGTGG
 Consensus   (551) CCCCAACC GGGCC  AAG  CCGC  CAAGGGCGGCTACTTCCCAGTGG
                   601                                            650
      2247   (569) CA---CCATACGACCAAACCGTTGACGTGCGCGATGACATGGTTCGGCAACC
     13032   (569) CA---CCATACGACCAAACCGTTGACGTGCGCGATGACATGGTTCGGCAACC
  CEFgInA1   (569) CA---CCCTACGACCAGACCGTGGACGTCCGCGATGAGATGGTCCGGCAACC
  CEFgInA2   (578) CA---CCCTATGACCACTTCCAGGACCTGCGCGACACCATTGGTGAGACCC
  MtugInA2   (479) CG---GTGCACGACTCCGCCTTGAACTTTCGCCGCCACGCGATCGATGCCC
  MtugInA3   (488) TG---CTCGAGCACGAGGCGTTCG---TCCGCGATGTCAACGCCGCGGCAA
  MtugInA4   (545) CATCCTCGCGGATGGAGCCGTTG--CTGCGCGACATCCGGTTGGGTA---
  MtugInA1   (569) GC---CCCAACGACCAATACGTCGACCTGCGCGACAAGATGCTGACCAACC
 Consensus   (601) CA  CCCTACGACCAA CCGT GAC TGCGCGATGACATGGT GGCAACC
                   651                                            700
      2247   (617) TCGGCAGCTTCCGGCTTCGCTCTTGAGCGTTTCCACCACGAAGTCGG---T
     13032   (617) TCGGCAGCTTCCGGCTTCGCTCTTGAGCGTTTCCACCACGAAGTCGG---T
  CEFgInA1   (617) TGCGTGACGCCGGTTTCCACCTGGAGCGTTTCCACCACGAGGTCGG---T
  CEFgInA2   (626) TGGCGGAGATCGGCGTTCACCCGTGGAGCGTTCCCACCATGAGATGGGCAGT
  MtugInA2   (527) TGGAATTCATGGGCATCTCGGTGGAGTTCAGCCATCACGAAGGCGC---A
  MtugInA3   (533) CGGCAG---CAGGCATCGCTATCGAGCAGTTCCATCCCGAATACGG---T
  MtugInA4   (590) TGGCCGGTGCGGGTCTGCGGATTCGAGGCGGTCAAAGGCGAATGCAA---C
  MtugInA1   (617) TGATCAACTCGCGGCTTCATCCTGGAGAAGGGCCACCACGAGGTGGGCAGC
 Consensus   (651) TGGCAG  CCGGCTTC C CTGGAGCGTTTCCACCACGAAGTCGG    T
                   701                                            750
      2247   (664) GGCGGACAGCAGGAAATCAACTACCGCTTCAACACCATGCTCCACGCGGC
     13032   (664) GGCGGACAGCAGGAAATCAACTACCGCTTCAACACCATGCTCCACGCGGC
  CEFgInA1   (664) GGCGGCCAGCAGGAGATCAACTACCGCTTCAACACCCTCCTGCACGCAGC
  CEFgInA2   (676) GGTGGTCAGCAGGAGATCAACTACCGTTTCAACACCGTGCTGCGGCGCAGC
  MtugInA2   (574) CCCGGCCAGCAGGAGATCGACCTGCGGGTTTGCGGACGCTCTGTCGATGGC
  MtugInA3   (577) GCCAACCAATTCGAGATCTCGTTAGCGCCGCAGCCGGCCGGTCGCGGCCGC
  MtugInA4   (637) ATGGGCCAGCAGGAGATCGGGTTTCGTTACGACGAGGCGCTGGTCACCTG
  MtugInA1   (667) GGCGGACAGGCGCGAGATCAACTACCAGTTCAATTCGCTGCTGCACGCGC
 Consensus   (701) GGCGGCCAGCAGGAGATCAACTACCG TTCAACACCCTGCTGCACGC GC
                   751                                            800
      2247   (714) AGATGATATCCAGACCTTCAAGTACATCATCAAGAACACCGCTCGGCCTCC
     13032   (714) AGATGATATCCAGACCTTCAAGTACATCATCAAGAACACCGCTCGGCCTCC
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3

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CEFglnA1   (714)  CGATGACATTCAGACCTTCAAGTACATCGTGAAGAACACCGCAGCCCTGC
CEFglnA2   (726)  CGATGACCTCCAGACCTTCAAGTACGTGGTGAAGAACACCGCGAAGGCCG
MtuglnA2   (624)  TGACAACGTGATGACCTTCCGCTACGTCATCAAAGAAGTCGCGCTGGAAG
MtuglnA3   (627)  CGATCAGCTGGTGCTGACCCGCCTCATCATCGGCCGTACCGCCCGCCGGC
MtuglnA4   (687)  CGACAACCATGCGATCTACAAGAACGCGCCAAGCGAAATCGCCGACCAGG
MtuglnA1   (717)  CGACGACATGCAGTTGTACAAGTACATCATCAAGAACACCGCCTGGCAGA
Consensus  (751)  CGATGACAT CAGACCTTCAAGTACATCATCAAGAACACCGC CGCC GC
                  801                                              850
2247       (764)  ACGGCAAGGCTGCAACCTTCATGCCTAAGCCACTGGCTGGCGACAACGGT
13032      (764)  ACGGCAAGGCTGCAACCTTCATGCCTAAGCCACTGGCTGGCGACAACGGT
CEFglnA1   (764)  ACGGCAAGGCTGCCACCTTCATGCCCAAGCCGCTGGCCGGTGACAACGGC
CEFglnA2   (776)  TCGGTAAATCCGCCACCTTCATGCCCAAGCCGCTGGCTGATGACGGCGGT
MtuglnA2   (674)  AGGGCGCCCGGGCGTCGTTCATGCCCAAGCCATTCGGCCAGCACCCGGGC
MtuglnA3   (677)  ACGGGTTACGCGTGAGCCTATCGCCAGCGCCCTTCGCCGGAAGTATCGGA
MtuglnA4   (737)  ACGGCAAGAGCCTAACGTTCATGGCGAA——ATACGATGAACGCGAAGGT
MtuglnA1   (767)  ACGGCAAACGGTCACGTTCATGCCCAAGCCGCTGTTCGGCGACAACGGG
Consensus  (801)  ACGGCAAG C GC ACCTTCATGCCCAAGCCACTGGCTGG GACAACGGT
                  851                                              900
2247       (814)  TCCGGCATGCACGCTCACCAGTCCCTCTGGAAGG———ACGGCAAGCCACT
13032      (814)  TCCGGCATGCACGCTCACCAGTCCCTCTGGAAGG———ACGGCAAGCCACT
CEFglnA1   (814)  TCCGGCATGCACGCCCACCAGTCCCTGTGGAAGG———ACGGCAAGCCACT
CEFglnA2   (826)  TCCGGCATGCACATCCACCAGTCGCTGTGGAAGG———ACGGCAAGCCCCT
MtuglnA2   (724)  TCGGCGATGCACAGCCACATGAGCCTGTTCGAGGGTGATGTCAACGCGTT
MtuglnA3   (727)  TCCCGGTGCCCACCAACACTTCTCGCTGACTATGTCGGAAGGGAT——GCT
MtuglnA4   (784)  AATAGCTGTCACATCCATGTCTCGCTGCGTGGGCACGGATGGCTCCGCGGT
MtuglnA1   (817)  TCCGGCATGCACTGTCATCAGTCGCTGTGGAAGG———ACGGGGCCCCGCT
Consensus  (851)  TCCGGCATGCAC CCCACCAGTCGCTGTGGAAGG    ACGGCAAGCCGCT
                  901                                              950
2247       (861)  CTTCCACGATGA-GTCCGGCTACGCAGGCCTGTCCGACATCGCCCGCTAC
13032      (861)  CTTCCACGATGA-GTCCGGCTACGCAGGCCTGTCCGACATCGCCCGCTAC
CEFglnA1   (861)  CTTCCACGACGA-GTCCGGCTACGCCGGCCTGTCCGACATCGCCCGTTAC
CEFglnA2   (873)  CTTCCATGATGA-GGCCGGTTATGCCAACCTGTCGGAGATGGCCCGTCAC
MtuglnA2   (774)  CCACAGCGCTGATGATCCGCT——GCAG—CTGTCGGAAGTGGGTAAATCG
MtuglnA3   (774)  GTTCTCCGGTGG-GACTGGAGCAGCTGGCATGACCTCGGCCGGGGAGGCC
MtuglnA4   (834)  GTTTGCCGACAGTAACGGGCCGCACGG-CATGTCGTCGATGTTCCGCAGC
MtuglnA1   (864)  GATGTACGACGA-GACGGGTTATGCCGGTCTGTCGGGACACGGCCCGTCAT
Consensus  (901)  CTTCCACGATGA GACCGGCTACGC GGCCTGTCGGACATGGCCCG TAC
                  951                                              1000
2247       (910)  TACATCGGCGGCATCCTGCACCACGCAGGCGCTGTTCTGGCGTT-CACCA
13032      (910)  TACATCGGCGGCATCCTGCACCACGCAGGCGCTGTTCTGGCGTT-CACCA
CEFglnA1   (910)  TACATCGGTGGCATCCTCCACCACGCCGGTGCGGTCCTGGCGTT-CACCA
CEFglnA2   (922)  TATGTCGGTGGTCTGCTCAAGCATGCCCCCGCGGTGCTGGCTTT-CACCA
MtuglnA2   (820)  TTCATCGCCGGGATCCTGGAGCACGGCTTGCGAGATCAGCGCGGT-CACAA
MtuglnA3   (823)  GCGGTCGGCAGGAGTGCTTC-GCGGACTACCGGACGCCCAAGGCATCCTGT
MtuglnA4   (883)  TTCGTCGCCGGCCAGTTGG-CCACGTTGCGCGCGAATTCACGGCTGTGCTATG
MtuglnA1   (913)  TACATCGGCCGGCCTGTTTACACCACGCGCCGTCGCTGCTGGCTTT-CACCA
Consensus  (951)  TACATCGGCGGCATGCTGCACCACGC GGCGCGGT CTGGCGTT CACCA
                  1001                                             1050
2247       (959)  ACGCAACCCTGAACTCCTACCACCGTCTGGTTCCAGGCTTCGAGGCTCCA
13032      (959)  ACGCAACCCTGAACTCCTACCACCGTCTGGTTCCAGGCTTCGAGGCTCCA
CEFglnA1   (959)  ACCCGACCCTGAACTCCTACCATCGCCTGGTGCCGGGCTTCGAGGCCCCC
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CEFgInA2   (971)  ACCCGACCCTGAATTCCTACAACCGTCTGGTGCCCGGTTTCGAGGCCCCG
MtugInA2   (869)  ATCAGTGGGTCAACTCTTACAAGCGGCTGGTGCAGGGCGGCGAAGCGCCC
MtugInA3   (872)  GCGGATCGATCGTGTCCGGTCTGCGAATGCGACCCGGTAACTGGGCCGGA
MtugInA4   (932)  CGCCGACCATTAACTCCTACAAGCGATTTGCCGATAGCAGTTTCGCGCCG
MtugInA1   (962)  ACCCGACGGTGAACTCCTACAAGCGGCTGGTTGCCGGTTACGAGGCCCCG
Consensus (1001)  ACCCGACCCTGAACTCCTACCAGCG CTGGT CC GGCTTCGAGGCCCC
                  1051                                           1100
2247      (1009)  ATCAACCTGGTGTACTCACAGCGCAACCGTTCCGCTGCTGTCCGTATCCC
13032     (1009)  ATCAACCTGGTGTACTCACAGCGCAACCGTTCCGCTGCTGTCCGTATCCC
CEFgInA1  (1009)  ATCAACCTGGTCTACTCCCAGCGCAACCGCTCGGCGGCCGTGCGTATCCC
CEFgInA2  (1021)  GTGAGCCTGGCGTATTCGCAGCAGAACCGTTCCGCCGCGATCCGCATTCC
MtugInA2   (919)  ACGGCCGCGTCGTGGGGGGGCCGCCAACCGATCCGCCCTAGTGCGGGGTGGC
MtugInA3   (922)  ATCTATGCATGCTGGGGGTACCGAAAACCGGGAAGCGGCGGTGCCGATTCGT
MtugInA4   (982)  ACGGCGCTGGCTTGGGGGCTGGACAATCGCACCTGCGCCCTGCGGGTTG--
MtugInA1  (1012)  ATCAACCTGGTCTATAGCCAGCGCAACCGGTCGGCATGCGTGCGCATCCC
Consensus (1051)  ATCAACCTGGTGTA TG CAGCGCAACCG TCCGC GC GTGCG ATCCC
                  1101                                           1150
2247      (1059)  AAT----CACCGGATCCAACCCGAAAGGCAAAGCGCATCGAATTCCGCGCTC
13032     (1059)  AAT--CACCGGATCCAACCCGAAGGCAAAGCGCATCGAATTCCGCGCTC
CEFgInA1  (1059)  GAT--CACCGGTTCCAACCCGAAGGCCAAGCGCATCGAGTTCCGCGCAC
CEFgInA2  (1071)  GGC--CAGCGGTCCCAACCCGAAGGGCGACCCGCATCGAGTTCCGCACCC
MtugInA2   (969)  GATGTACACGCCGCACAAGACCTCGTCGCGGCGGGGTCGAAGTACGCAGCG
MtugInA3   (972)  CAAGGGCGGGGGCTGGCAGCGCGGTACGGCGGGAACGTGGAGGGTGAAGGTCG
MtugInA4  (1030)  GTTGGCCACGGG----CAAAACAT---C------CGGGTCGAATGCCGGGTTC
MtugInA1  (1062)  GAT----CACCGGCAGCAACCCGAAGGCCAAGCGGCTGGAGTTCCGGAAGCC
Consensus (1101)  GAT   CACCGG  CCAACCCGAAGGC AAGCGCATCGAGTTCCGCGCCC
                  1151                                           1200
2247      (1106)  CAGACCCATCAGGCAACCCATACCTGGGCTTCGCAGCGATGATGATGGCC
13032     (1106)  CAGACCCATCAGGCAACCCATACCTGGGCTTTGCAGCGATGATGATGGCC
CEFgInA1  (1106)  CGGACCCATCCGGCAACCCCTACCTGGGCTTCGCCGCCATGATGATGGCC
CEFgInA2  (1118)  CGGACCCCTCGGGTAACCCCTACCTGGCGTTCACCGCGTCGATGATGGCG
MtugInA2  (1019)  CTGATTCGGCGTGCAATCCCTATCTGACATTCCCCGTGCTGCTGGCCGCG
MtugInA3  (1022)  TCGACCCGTCGGGCCAACCCGTATCTCGCGTCGCGCGGCGATCCTCGGACTG
MtugInA4  (1070)  GCGGCGGTGATGTCAACCAGTACCTGGCGGTTGGCGGCTCTTCATTGCTGGA
MtugInA1  (1109)  CCGACTCGTCGGGCAACCCGTATCTGGCGTTCTCGGCCCATGCTGATGGCA
Consensus (1151)  C GACCC TCGGGCAACCC TACCTGGCGTTCGC GCGATGATGATGGC
                  1201                                           1250
2247      (1156)  GGCCTCGACGGCATCAAGAACCGCATCGAGCCACACGCTCCAGTGGACAA
13032     (1156)  GGCCTCGACGGCATCAAGAACCGCATCGAGCCACACGCTCCAGTGGACAA
CEFgInA1  (1156)  GGCCTGGACGGTGTGAAGAACCGCATCGAGCCGCACGCACCGGTGGACAA
CEFgInA2  (1168)  GGCCTGGACGGCATCCGCAACCGCATCGAACCCGACGCCCTCTGGACAA
MtugInA2  (1069)  GGATTGCGGGGGTGTAGAGAAGAGGGTTACGTGCTGGGCCCGCAGGCCGAGGA
MtugInA3  (1072)  GCACTCGACGGCATGAAGACCAAGGCGGTGTTGCCGTCGGAAACGACCGT
MtugInA4  (1120)  GGGTTGTACGGTATCGAGCGGGGCCTTCAGCTGCCCGAGCCCTGTGTCGG
MtugInA1  (1159)  GGCCTGGACGGTATCAAGAACAAGATCGAGCCGCAGGCGCCCGTCGACAA
Consensus (1201)  GGCCTGGACGGTATCAAGAACCGCATCGAGCCGCACGCGCC GTGGACAA
                  1251                                           1300
2247      (1206)  GGACCTCTACGAACTGCCACCAGAGGAAGCTGCATGCAT------TCCAC
13032     (1206)  GGACCTCTACGAACTACCACCAGAGGAAGCTGCATCCAT------TCCAC
CEFgInA1  (1206)  GGACCTCTACGAGCTCCCACCGGAGGAGGCCGCCTCCAT------CCCGC
CEFgInA2  (1218)  GGACCTCTATGAGCTCCCGCCCGAGGAGGCTGCCAAGGT------CGCCG
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MtuglnA2  (1119) CAACGTATGGGACCTCACACCCGAGGAACGCCGAGCGATGGGGTACCGAG
MtuglnA3  (1122) AGACCCGACACAGCTGTCTGACGTGGATCGTGACCGTGCCGGCATTCTGC
MtuglnA4  (1170) CAACG-------CCT--ACC-----AAGGCGCCGATGT------CGAAC
MtuglnA1  (1209) GGATCTCTACGAGCTGCCGCCGGAAGAGGCCGCGAGTAT------CCCGC
Consensus (1251) GGACCTCTACGAGCT CCACC GAGGAAGCTGCC C AT      CCCAC
                 1301                                             1350
     2247 (1250) AGGCACCAACCTCCCTGGAAGCATCCCTGAAGGCACTGCAGGAAGACACC
    13032 (1250) AGGCACCAACCTCCCTGGAAGCATCCCTGAAGGCACTGCAGGAAGACACC
 CEFglnA1 (1250) AGGCACCGACCTCCCTGGAGGCATCCCTGAAGGCCCTGCAGGACGACTCC
 CEFglnA2 (1262) AGGCCCCACCTCACTGGAACAGGCGCTGAAGGCCCTGGAGGACGGACCAC
 MtuglnA2 (1169) AATTGCCGTCCAGTTTGGATAGTGCGCTGCGCGCCATGGAGGC---CTCC
 MtuglnA3 (1172) GACTTGCTGCCGATCAGGCGGATGCAATTGCTGTACTGGATAG---TTC
 MtuglnA4 (1199) GGCTGCCGGTTACGCTGGCCGACGCCGCGGTGCTGTTCGAGGA---TTCT
 MtuglnA1 (1253) AGACTCCGACCCAGCTGTCAGATGTGATCGACCGTCTCGAGGCCGACCAC
Consensus (1301) AGGC CCGACCTC CTGGAAGA GCCCTGAAGGC CTGGAGGA GACTCC
                 1351                                             1400
     2247 (1300) GACTTCCTCACCGAGTCTGACGTCTTCACCGAGGATCTCATCGA-GGCGT
    13032 (1300) GACTTCCTCACCGAGTCTGACGTCTTCACCGAGGATCTCATCGA-GGCGT
 CEFglnA1 (1300) GACTTCCTCACCGAGTCCGACGTGTTCACCGAGGACCTCATCGA-GGCCT
 CEFglnA2 (1312) GAGTTCCTCACCGAGGGTGACGTGTTCACCGATGATCTCATCGA-GGCCT
 MtuglnA2 (1216) GAACTCGTCGCGGAG-------GCCTTGGGGGAGCACGTTTTTGA-CTTTT
 MtuglnA3 (1218) GAAACTGCTTCGGTG-------CATCCTTGGCGATCCCGTGGTAGATGCCGT
 MtuglnA4 (1246) GCGCTGGTGCGCGAG-------GCGTTCGGCGGAGGATGTTGTGGC-GCACT
 MtuglnA1 (1303) GAATACCTCACCGAAGGAGGGGTGTTCACAAACGACCTGATCGA-GACGT
Consensus (1351) GA TTCCTCACCGAG      GACGTGTTCACCGAGGATCTCATCGA GGCGT
                 1401                                             1450
     2247 (1349) ACATCCAGTACAAGTAC--GACAACGAGATCTCCCCAGTTCGCCTGCGC
    13032 (1349) ACATCCAGTACAAGTAC--GACAACGAGATCTCCCCAGTTCGCCTGCGC
 CEFglnA1 (1349) ACATCCAGTACAAGTAC--GACAACGAGATCACCCGGGTCGCCTGCGC
 CEFglnA2 (1361) ATGTGGCCTACAAGCAT--GAACATGAGATCACCCGTGAGCGTCTGCGC
 MtuglnA2 (1259) TCTTGCGCAACAAGCGCACGGAGTGGGCGAACTACCGGCAGCCACGTCACG
 MtuglnA3 (1263) GGTCGCGGTACGCCAGT-TAGAGCATGAGCGCTAC----GGTGACCTCGAT
 MtuglnA4 (1289) AGCTGAACAACGCGCGTGTGGAGCTGGCGGCGTTCAACGCGGCGGGTCA--
 MtuglnA1 (1352) GGATCAGTTTCAAGCGC--GAAAACGAGATCGAGCCGGTCAACATCCCGG
Consensus (1401) ACATGCAGTACAAGCGC  GA AACGAGATCTCCCC GT CGCCTGCGC
                 1451                              1495
     2247 (1396) CCAACCCCGCAGGAATTCGAATTGTACTTCGACTGC-------
    13032 (1396) CCAACCCCGCAGGAATTCGAATTGTACTTCGACTGCTAA-----
 CEFglnA1 (1396) CCCACCCCGCAGGAGTTCGAGCTGTACTTCGACTGCTAG------
 CEFglnA2 (1408) CCCACCGCTCTGGATTTCGAGCTGTACTACGACTGCTAG------
 MtuglnA2 (1309) CCATACGAGCTGCGCACCTACCTGTCGCTGTAG-----------
 MtuglnA3 (1309) CCTGCGCAGCTGGCCGACAAGTTCCGGATGGCTTGGAGTGTGTAA
 MtuglnA4 (1337) CCGATTGGGAGAGGATACGTGGATTTGAGCGCCTCTAG-------
 MtuglnA1 (1399) CCGCATCCCTACGAATTCGCGCTGTACTACGACGTTTAA------
Consensus (1451) CC ACCCCGCAGGAATTCGAGCTGTACTTCGACTGCTA
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2247 : B. flavum ATCC14067
13032：C. glutamicum ATCC13032
CEF: C. efficiens YS314
Mtu: Mycobacterium tuberculosis H37RV

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